


```

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51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisIleGlyThrTy 67
168 CTGTGACAAATCACTGTCCAGCCGCGCGGACAGGAACCGACTGCGAGG 217
.....
67 ThrLeuValAsnAspCysTrGlyTrGlyGlnAspThrAspCysArgGln 84
218 ATCAAAATATATATATATATATATATATATATATATATATATATAT 267
.....
84 YsGluSerGlySerPheThrAlaSerGlnAsnHisGlnArgHisCysLeu 130
268 AGCTGCTCCAAATGCTCAAAAGGAAATGGGTTCAGCTGGACATGCTCTG 317
.....
101 SerGlySerLysCysArgLysGlnAsnGlyGlnValGlnLysSerSer 117
318 CACATTCAGACGCGAATACGCGCGCGCGCGCGCGCGCGCGCGCGCG 467
.....
117 ThrValAspArgAspThrValCysGlyCysArgGlyAsnGlnIleTargH 134
368 ATTATTGAGTGAAGAACTTTTCATGATGCTCAATTCACAGCTCTGCTG 417
.....
134 IstYrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
418 AATGGGACGCGCACCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 467
.....
151 AsnGlyThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 167
468 CTGCTCATCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 517
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167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
518 ACTGTAAATAAGGATGATGATGATGATGATGATGATGATGATGATGAT 567
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568 AATGCTAAGGCGCTGAGGACTGAGGCGAGGCGAGGCGAGGCGAGGCG 600
.....
201 AsnValCysGlyThrGlnAspSerGlyThrThr 211

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seq_name: US-09-525-998a-11.rag; seq_id: 11; seq_len: 600; seq_desc: 11 x AA89224

seq_documentation_block:

ID: AA89224 standard; Protein: 420 AA.

AC: AA89224:

DI: 04-MAR-1999 (first entry)

LE: Tumour necrosis factor bp/osteoprotegerin construct, INHBP/OPG.

KW: Tumour necrosis factor receptor 1; TNFR-1; inhibitor: osteoprotegerin;

OPG; chimeric fusion dimerisation domain; autoimmune disease;

inflammation; apoptosis.

OS: Homo sapiens.

PS: Synthetic.

XX: W09849305-A1.

XX: 05-NOV-1998.

XX: 29-APR-1998: 9404-150631

XX: 01-MAY-1997: 47US-08501RR

XX:

PA (AMGP-) AMGN INC.

PI Boyle WJ, Wooden S;

XX WPI: 1999-034661/94.

XX New chimeric osteoprotegerin polypeptides contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence.

PT useful to treat TNF and TNFR-mediated disorders.

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (i) a multimer polypeptide
 CC comprising covalently associated A1 molecules, (ii) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressed. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC at least one of A1, A1R, A1S and A1L are also described. A1, A1R, A1S and
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFR-1/3 construct from
 CC the example of the present invention for creating TNFR/OPG fusion
 CC proteins.

XX Sequence 420 AA:

alignment_scores:

Quality: 1117.50 Length: 211

Ratio: 5.588 Gaps: 1

Percent Similarity: 94.787 Percent Identity: 94.787

alignment_block:

US-09-525-998A-11 x AA89224

Align seq 1/1 to: AA89224 from: 1 to: 420

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1 ATGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 50
|||||
1 MetGlyLeuSerThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 17
|||||
67 ThrValAspArgAspThrValCysGlyCysArgGlyAsnGlnIleTargH 60
|||||
17 MetGlyLeuSerThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 34
|||||
88 .....GATAGTGTGTGTCGCCAAGGAAAAATATATC 117
|||||
34 euGlyAspArgGlnLysArgAspSerValCysTrGlyGlnGlyTyrIle 50
|||||
118 CACCTCAAAATAATTCAGATTCGTCATCAAGTGGCAAAATAAATCA 147
|||||
51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisIleGlyThrTy 67
|||||
168 CTGTGACAAATCACTGTCCAGCCGCGCGGACAGGAACCGACTGCGAGG 217
|||||
67 ThrLeuValAsnAspCysTrGlyTrGlyGlnAspThrAspCysArgGln 84
|||||
218 ATCAAAATATATATATATATATATATATATATATATATATATATAT 267
|||||
84 YsGluSerGlySerPheThrAlaSerGlnAsnHisGlnArgHisCysLeu 100
|||||
268 AGCTGCTCCAAATGCTCAAAAGGAAATGGGTTCAGCTGGACATGCTCTG 317
|||||
101 SerGlySerLysCysArgLysGlnAsnGlyGlnValGlnLysSerSer 117
|||||
318 CACATTCAGACGCGAATACGCGCGCGCGCGCGCGCGCGCGCGCGCG 467
|||||

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